

FIG.1

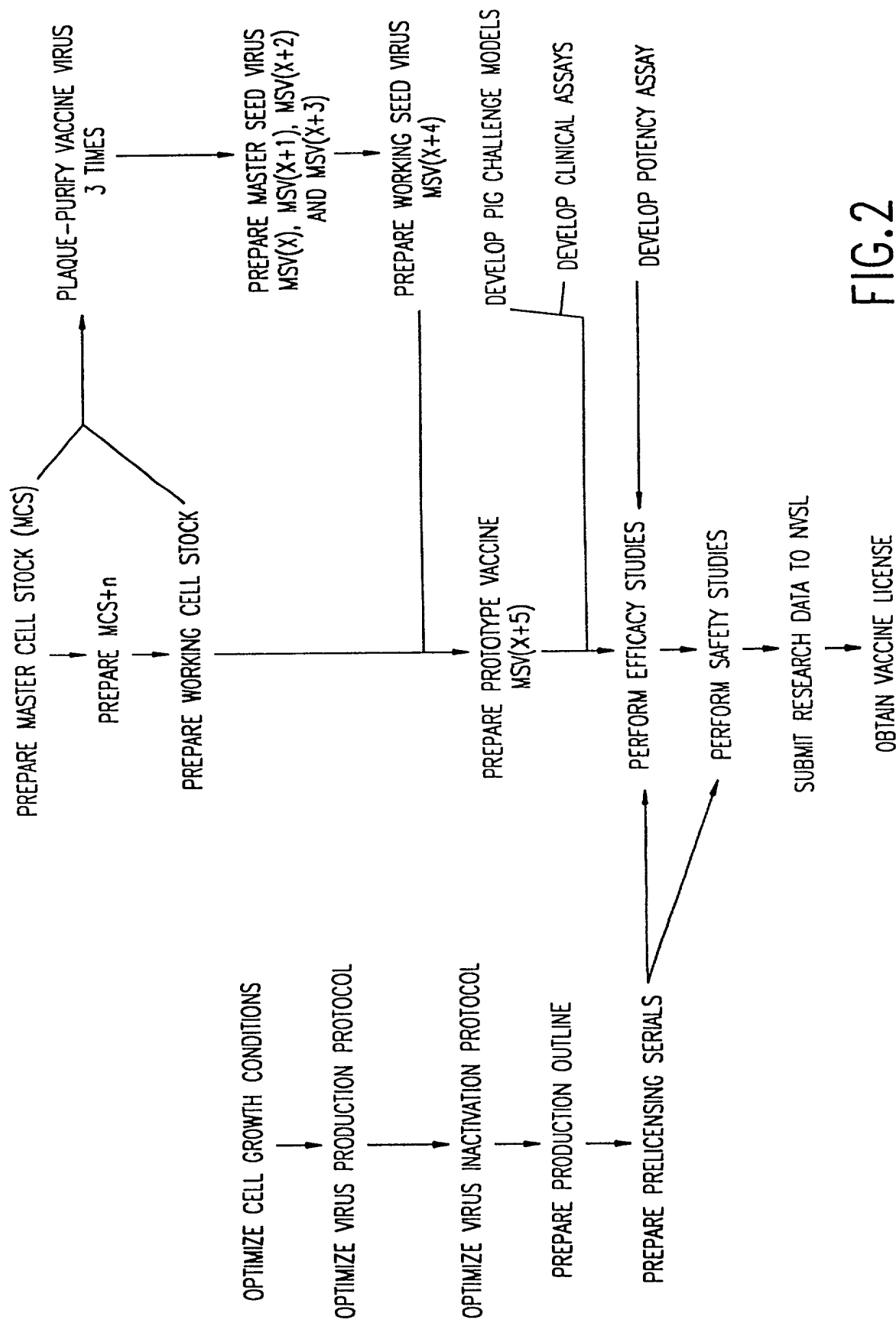


FIG.2

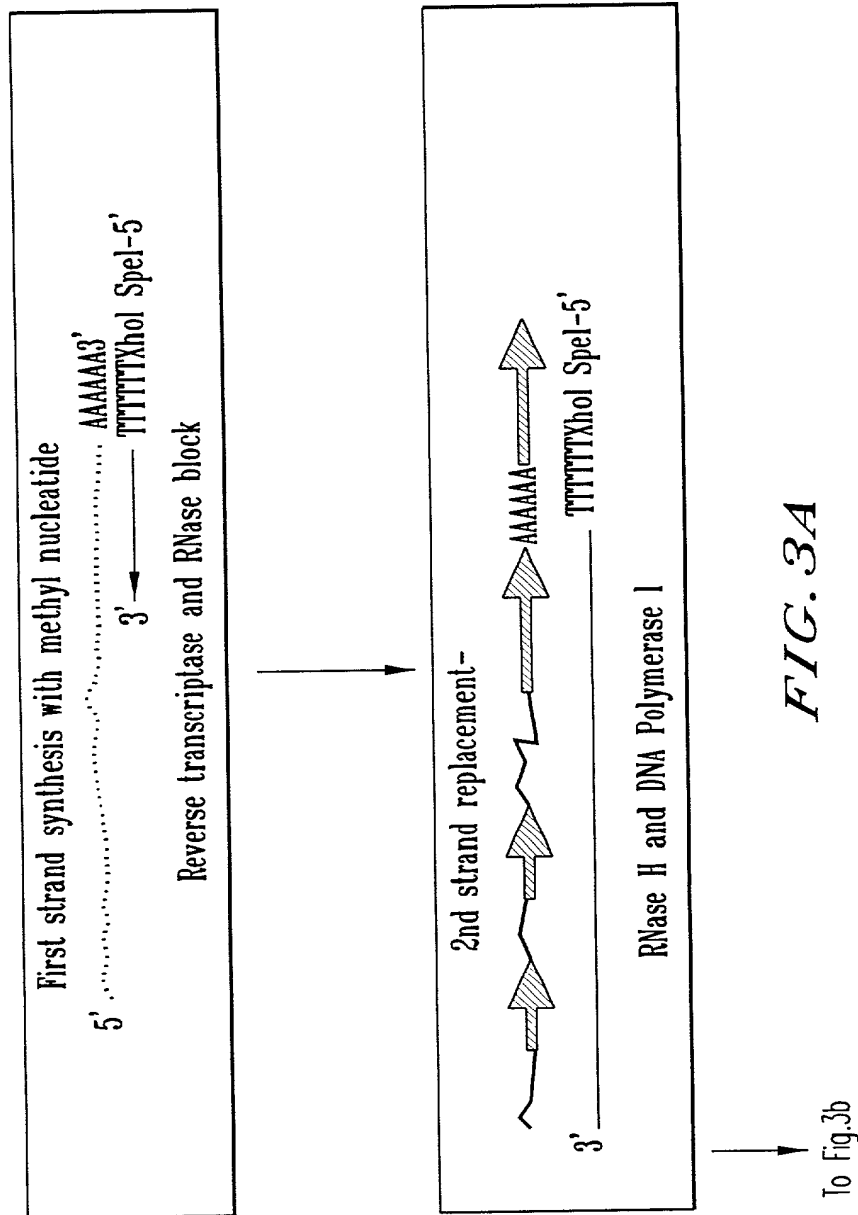


FIG. 3A

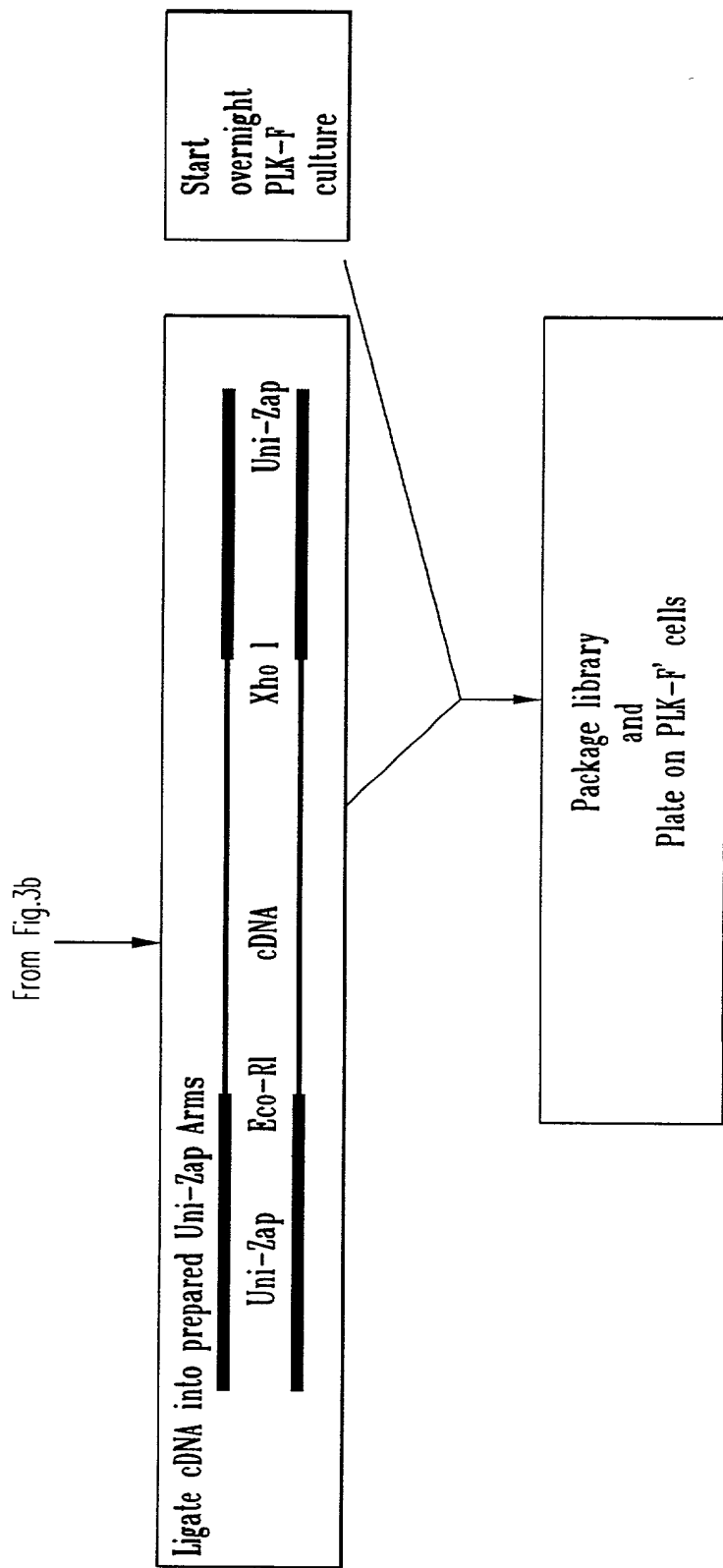


FIG. 3c

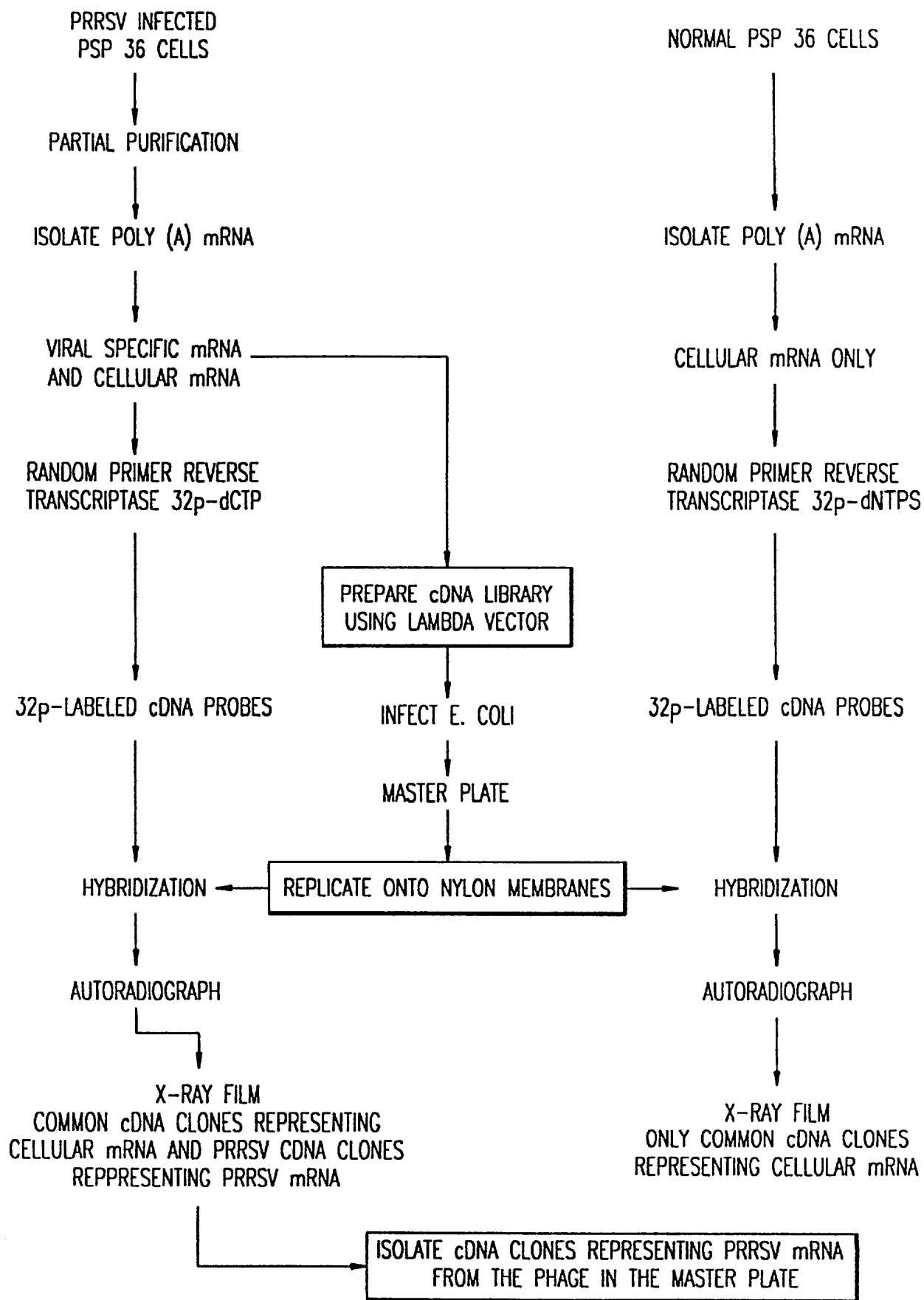


FIG.4

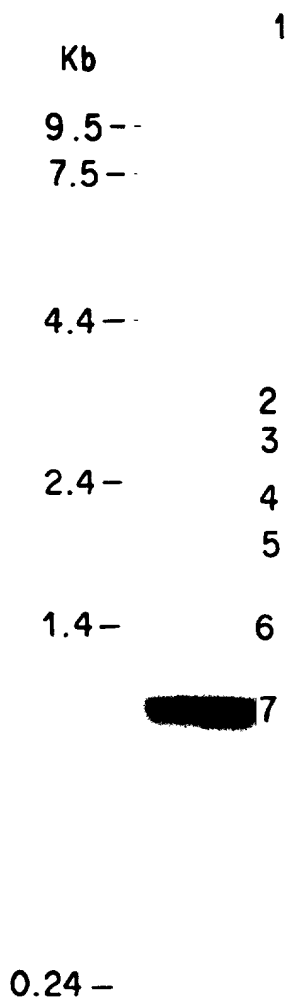


FIG.5

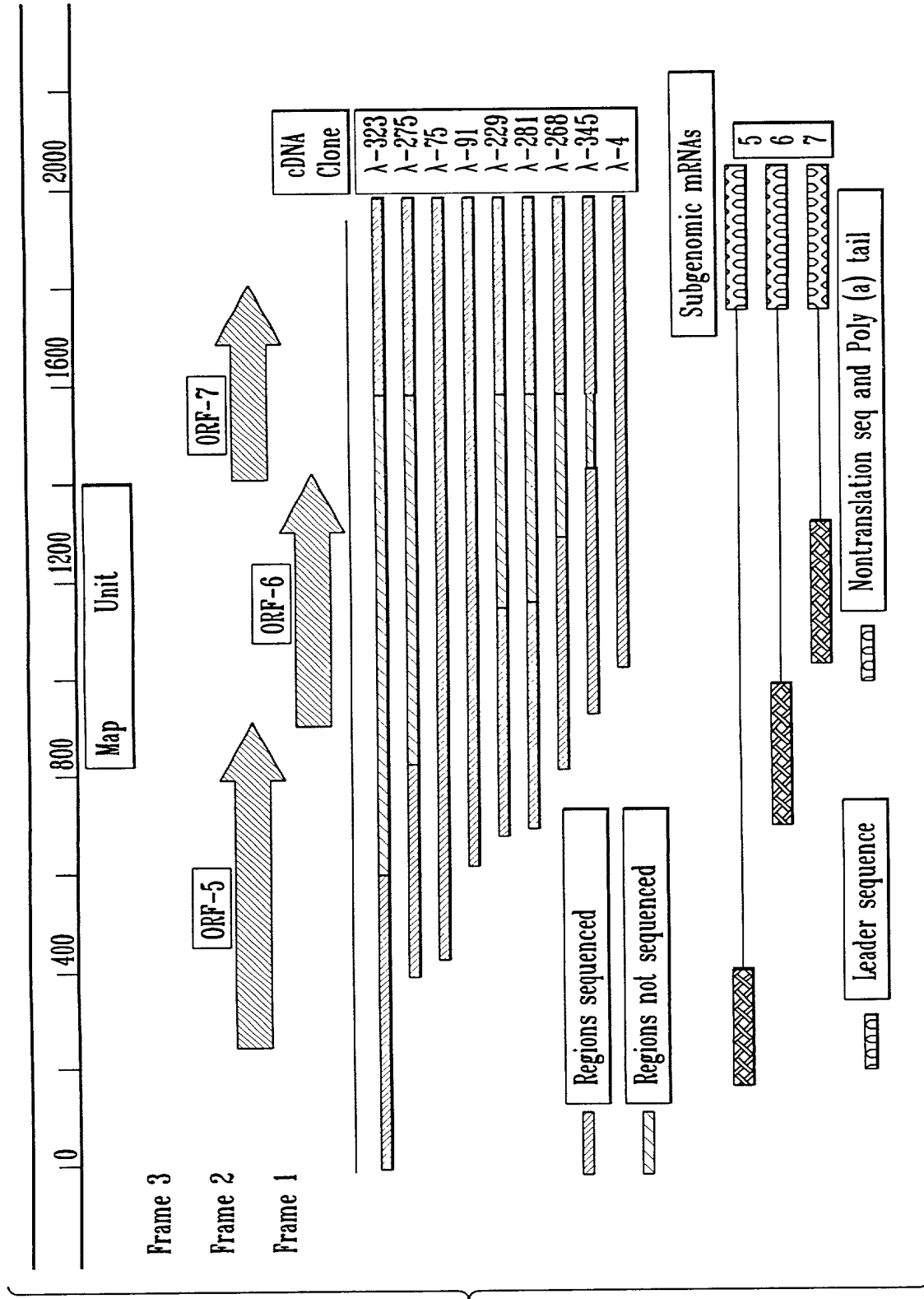


FIG. 6

GGCAGGCTTGGCTGCTCCAAAGACATCAGTTGCCCTAGGCCATCGCAACTCGGCCCTCGAGGCGATTGGCAAAAGTCCCTCAGTGGCGCACGGCGGATAGGG 100
 ACACCGGTGATATCACTGTCACAGCCAAATGTTACCGATGAGAAATTATTGGCATTCCTCTGATCTTCTCATGCTTCTTCTTGCCCTTTTCTATGCTTCTG 200
 AGATGAGTGAAGAAGGGATTAAAGGTGGTATTTGGCAATGTCAGGCATCGTGGCAGTGGCGTCAACTTACCAGTTACGTCCACATGTC AAGGAATT 300
 TACCCAACGTTCCCTGGTAGTTGACCATGTGCGGCTGCTCCATTTCATGACGCCGAGACCATGAGGTGGGCAACTGTTTTAGCCTGCTCTTTTGGCATT 400
 DRF4 stop
 *** +1>DRF5 start
 CTGTTGGCAATTTGAATGTTAAGTAGTTTGGGGAAATGCTTGACCGGGGCTGTTGCTCGCAATTGCTTTTTTGGGTGATCGTGGCGTCTTGTTTT 500
 GTTGGCTCGTCAGCGCCACAGGGACAGCGGCTCAAATTTACAGCTGATTTACAACTTGACGCTATGTGAGCTGAATGGCACAGATTGGCTAGCTAATA 600
 AATTGACTGGCAGTGGAGTGTTTGTGCATTTTTCCGTGTTGACTCACATTGCTCTTATGGTGCCCTCACACTACTAGCCATTCCCTTGACACAGTCGG 700
 TCTGGTCACTGTGCTACCGCTGGGTTTGTTCACGGGGGTAIGTTCTGAGTAGCATGTACGGCGTCTGTGCCCTGGCTGGCTTGATTGCTTCGTCATT 800
 AGGCTTGCAGAGAAATTGCATGTCTCTGGGCTACTCATGTACCAGATATACCAACTTCTTCTGGACACTAAGGGCAGACTCTATCGTTGGCGGTGGCCTG 900
 TCATCATAGAGAAAAGGGCAAGTTGAGGTGGAAGGTCACCTGATCGACCTCAAAAGAGTTGTGCTTGATGGTTCGGCGGTACCCCTGTAAACCAGAGT 1000
 DRF6 start
 +1> ***DRF5 stop
 TTCAGCGGAACAATGGAGTCGTCCTTAGATGACTTCTGTGTCATGATAGCAGGGCTCCACAAAGGTGCTCTTGGCGTTTTTCTATTACCTACACGCCAGTGA 1100

FIG. 7A

TGATATATGCCCTAAAGGTAGTCGGCGCGGACTGCTAGGGCTTCGACCTTTTGGCTTCCTGAAATGGTGTTCACCTTCGGGTACATGACATTCGT 1200
 GCACCTTCAGAGTACAAATAAGGTGCGGCTCAGTATGGGAGCAGTAGTTGCACCTCCTTTGGGGGGTGTACTCAGCCATAGAAACCTGGAAATTCATCACC 1300
 TCCAGATGCCGTTTGTGCTTGCTAGGCGCGCAAGTACATTCTGGCCCCCTGCCACCACGTTGAAAGTGC CGCAGGCTTTCATCCGATTGCGGCAATGATA 1400
 ACCACGCATTTGTGCTCCGGGCTCCACTACGGTCAACGGGCACATTGGTGGCCCGGGTTAAAAAGCCTCGTGTGGGTGGCAGAAAAGCTGTAA 1500
 ACCAGGGAGTGGTAAACCTTGTAAATATGCCAAATAACACCGGCAAGCAGAGAGAGAGAAAGAGGGGATGGCCAGCCAGTCAATCAGCTGTGCCAGAT 1600
 GCTGGGTAAAGTATCGCTACCAAAACCAGTCCAGAGGCAAGGGACCGGGAAGAAAAAATAAGAGAAAAACCCGGAGAGCCCCCATTTCCCTCTAGCG 1700
 ACTGAAGATGATGTCAGACATCATTACCCCTAGTGAGGTCATTTGTGCTGTGTCATCCAGACCGCCTTTAATCAAGGGCGCTGGGACTTGCACCC 1800
 TGTGAGATTGAGGGAGGATAAGTTACACTGTGGAGTTAGTTTGCTACGCATCATACTGTGGCCCTGATCCGGGTCACAGCATCACCCCTCAGCATGATG 1900
 GGTGGCATTCCTGAGGCATCCAGTGTGTAATTGGGAAGATGCGTGGTGAATGGGACTGATTGACATTGTGCCCTTAAGTCACCTATTCAATTAGGGC 2000
 GACCGTGTGGGGTAAGATTTAATTGGCGAGAACACACGCGCGAAATTAATAAAAAAAAAAAAA 2062

RF7 start

+1> ***RF6 stop

***RF7 stop

FIG. 7B

LELYSTAD SEQ (13484-14089)	ATGAGATGTTCTCACAAATGGGGCGTTCTTGACTCCGCACCTCTTGGCTCTGGTGGCTTTTTTTCGTGGTA--	13556
ISU-12-3' TERMINAL (426-1028)	-----ATGTTGGGAAATCTTGACCGCGGCTGTGGCTCGCAATTTGGCTTTTTTGTGGGTATC	485
LELYSTAD SEQ (13484-14089)	---CCGCTTGTCTGTGTTCTTTGGGATGGCAACGGACAGCTCGACATACCAATTA--ATATATAAATTG	13624
ISU-12-3' TERMINAL (426-1028)	GTGCGCTCTTGTTTGTGGCTCGTACGGCCAACGGACAGCGGCTCAAAATTACAGCTGATTTACAACTTG	560
LELYSTAD SEQ (13484-14089)	ACGATATGGAGCTGAATGGACCGACTGGTTGTCCAGCCATTTTGGTGGGCAGTGGAGACCTTTGTGCTTTAC	13699
ISU-12-3' TERMINAL (426-1028)	ACGCTATGTGAGCTGAATGGACAGATTGGCTAGCTTAATAATTTGACTGGGCAGTGGAGTGTCTTGCTATTTT	635
LELYSTAD SEQ (13484-14089)	CCGGTTGCCACTCATATCCCTCTCAGCTGGTTTCTCACACACAGCCATTTTGTGACCGGCTCGGCTCTGGGCT	13774
ISU-12-3' TERMINAL (426-1028)	CGTGTGTGACTCAGATTGCTCTGTATGGTGGCTCAGTACAGCCATTTCCCTTGACACAGTCCGCTCTGGTCACT	710
LELYSTAD SEQ (13484-14089)	GATCCACTGGAGGATTGTTGGCGGGGGGTAGTACTCTGCAGGCTCTACGGGCTTGTGCTTTGGCAGCGGTTC	13849
ISU-12-3' TERMINAL (426-1028)	GTGCTACCGCTGGGTTGTTACAGGGGGGTATGTTCTGAGTAGCATGTACCGGCTGTGTGCCCTGGCTGGCTTG	785
LELYSTAD SEQ (13484-14089)	GATGTTTGTGATCCGTGCTGCTAAAAATTGGCATGGCTTCCGCGTATGCCGTACCGGTTTACCAACTTCATT	13924
ISU-12-3' TERMINAL (426-1028)	AATTTGCTTGGTCAATAGGCTTGGCAAGAAATTGCATGTCTTCCGCGTACTCATGTACCAATATACCAACTTTCTT	860
LELYSTAD SEQ (13484-14089)	GTGGACGACCGGGGAGAGTTTCATCGATGGAGTCTCCAAATAGTTGGTAGAAAAATTTGGGCAAGCCGAGTCCGAT	13999
ISU-12-3' TERMINAL (426-1028)	CTGGACACTAAGGGGAGACTCTATCGTTGGCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	935
LELYSTAD SEQ (13484-14089)	GGCAACCTCGTCACTCAAAACATGTGCTCTGAAAGGGTTAAAGCTCAACCCCTTACAGAGGACTTGGGTGA	14073
ISU-12-3' TERMINAL (426-1028)	GGTCACCTGATCGACCTCAAAAGAGTTGTCTTGTATGGTTCCGGGCTTACCCCTGTAAACAGAGTTTCAAGCGGA	1009
LELYSTAD SEQ (13484-14089)	GCAATGGGAGCCCTAG-----	14089
ISU-12-3' TERMINAL (426-1028)	ACAAATGGAGTGGTCCCTTAG	1028

FIG. 8

ISU 12/7a/3' terminal (888 – 1413) Lelystad seq (14077 – 14598)	AATGGAGTGG TCGTTACATG ACTTGTGTCA TGATAGACG GGTCCACAAA AGGTGCTCTT -ATGG-CAGG --CGTAGACG ATTGTGCAA CGATCCATATC GCGGCACAAA AGCTGGTGGT	947 14132
ISU 12/7a/3' terminal (888 – 1413) Lelystad seq (14077 – 14598)	GGGTTTCT ATTAACATACA CCGCAGTATGAT GATATATGCC CTAAAGGTGA GTCCGGGGCG ACCGTTTACC ATCACAATACA CACCTATTAAT GATATACGCC CTAAAGGTGT CACGGGGCGG	1007 14192
ISU 12/7a/3' terminal (888 – 1413) Lelystad seq (14077 – 14598)	ACTGCTAGGG CTCTGCACC TTTTGGTCTT CCTGAATTGT GCTTTCACCT TCGGGTACAT ACTCTCGGG CAGTTCACCA TCCTAATATTT TCTGAACCTGT TCGTTACAT TCGGATACAT	1067 14252
ISU 12/7a/3' terminal (888 – 1413) Lelystad seq (14077 – 14598)	GACATTCGTG CACTTTCAGA GTACAAATAA GTTCGGCTC ACTATGGGAG CAGTAGTTGC GACATATCTG CATTTTCAAT CCACCAACCG TGTCCGACTT ACCCTGGGGG CTGTTGTCG-	1127 14311
ISU 12/7a/3' terminal (888 – 1413) Lelystad seq (14077 – 14598)	ACTCTTTTGG GGGGTGTACT CAGC -CATTA GAACCTTGA ATTTATACAC CTCCAGATGC -CCCTTCTGT GGGGTGTCTTA CAGCTTCACA GAGTCATGGA AGTTTATCAC TTCCAGATGC	1185 14370
ISU 12/7a/3' terminal (888 – 1413) Lelystad seq (14077 – 14598)	CGTTTGTGCT TGTACGCCG CAAGTACATT CTGGCCCCCTG CCCACACGT TGAAGTGC AGATTGTGTT GCCTTGGCCG GCGATACATT CTGGCCCCCTG CCCATCACGT ACAAGTGT	1245 14430
ISU 12/7a/3' terminal (888 – 1413) Lelystad seq (14077 – 14598)	GCAGGCTTTC ATCCGATTGC GGCATAATGAT AACCAAGCAT TTGTGTCTCG GCGTCCGGC GCAGGCTCTC ATTATATCTC AGCGTCTGCT AACCGAGCAT AGCGTCTAG AAAGCCCGGA	1305 14490
ISU 12/7a/3' terminal (888 – 1413) Lelystad seq (14077 – 14598)	TCCACTAGG TCAACGGCAC ATTGGTCCC GGGTTAAAAA GCCTCGTGT GCGTGGCACA CTACATCAG TCAACGGCAC TGTAGTACCA GGAATTCGGA GCCTCGTGT GCGCGGCANA	1365 14550
ISU 12/7a/3' terminal (888 – 1413) Lelystad seq (14077 – 14598)	AAMGCTGTTA AACAGGAGT GGTAAACCTT GTTAATATG CCAAAATA CCAGCTGTTA AACGAGAGT GGTAAACCTC GTTAAGTATG GCGGTTAA	1413 14598

FIG.9

Lelystad seq (14588 – 14974)	ATGGCCGGTA AAAACCAAG- GCCAAGAAAGT A-CAG-----C 14632
ISU 12/7a/3' terminal (1403 – 1774)	-----AT GCCAATATAC ACCGCAACG ACACAAAGAG 1434
Lelystad seq (14588 – 14974)	TCCGATGGGG AATGGCCAGC CAGTCAATCA ACTGTGCCAG TTGCTGGGTG 14681
ISU 12/7a/3' terminal (1403 – 1774)	AAAGAGCGGG CATGGCCAGC CAGTCAATCA GCTGTGCCAG ATGCTGGGT- 1483
Lelystad seq (14588 – 14974)	CAATGATAAA GTCCACAGCC CACCAAGCTA GCGG--A-GG ACAGGCCAAA 14728
ISU 12/7a/3' terminal (1403 – 1774)	-AA-GATCAT CGCTCAGAA AACAGTCCA GAGGCAAGG ACCGG---GA 1528
Lelystad seq (14588 – 14974)	AAGAAAAA-- ----G----- -CCTGAGAAG CACATTITTC CCGTGGGTGG 14766
ISU 12/7a/3' terminal (1403 – 1774)	AAGAAAAATA AGAAGAAAAA CCGCGAGAAG CCGCATTTCC CTCIAGCGAG 1578
Lelystad seq (14588 – 14974)	TGAAGATGAC ATCCGGGACC ACCTACCCCA GACTGAACGC TCCGTCTGCT 14816
ISU 12/7a/3' terminal (1403 – 1774)	TGAAGATGAT GTACAGATTC ACTTTACCCC TAGTACCGGT CAAATTGTGTC 1628
Lelystad seq (14588 – 14974)	TCCAATTCAT CCAGACCGGT TTCAATCAAG GCGCAGGAAG -TGGCTGGCT 14865
ISU 12/7a/3' terminal (1403 – 1774)	TGTGTTAAT CCAGACCGCC TTTAATCAAG GCGCTGGGAG TTGCAAG-CT 1677
Lelystad seq (14588 – 14974)	TTTCATCCAGC GGAAGGTCA GTTTTCAGGT TGAGTTTATG CTGCGCGTTG 14915
ISU 12/7a/3' terminal (1403 – 1774)	GTCAGATTCA GGGAGGATTA GTTACACTGT GGAGTTTATG TTGCGTACGC 1727
Lelystad seq (14588 – 14974)	CTCATAAGT GCGCCCTGATTT CCGGTGACTT CTACATCCGC CAGTACGGGT 14965
ISU 12/7a/3' terminal (1403 – 1774)	ATCATACTGT GCGCCCTGATC CCGGTGACAG CATCACCG-T CAG-CATGA- 1774
Lelystad seq (14588 – 14974)	GCAAGTTAA 14974
ISU 12/7a/3' terminal (1403 – 1774)	1774

FIG.10

ISU 12/7a/3' terminal (1775 – 1938)	TGGGCTGGCA TTCTTGAGGC ATCCACTGT TTGAATTGGA	1814
Lelystad seq (14975 – 15101)	-----	14976
ISU 12/7a/3' terminal (1775 – 1938)	ACAAATGGCTG GTGAATGGCA CTGATTGACA TTGTGCCTCT	1854
Lelystad seq (14975 – 15101)	TGACAGTCAG GTGAATGGCC GCGATTGGCG TTGTGCCCTCT	15016
ISU 12/7a/3' terminal (1775 – 1938)	AAGTCACCTA TTCAATTAGG GCGACCTGT GGGGTTAGA	1800
Lelystad seq (14975 – 15101)	GAGTCACCTA TTCAATTAGG GCGATCACAT GGGGTTGATA	15056
ISU 12/7a/3' terminal (1775 – 1938)	TTTAAATT-GG GAGGAACCAC ACCTCCGAAA TTAAAAAAA	1933
Lelystad seq (14975 – 15101)	CTTAAATCAGG GAGGAACCAT GTTACCGAAA TTAAAAAAA	15096
ISU 12/7a/3' terminal (1775 – 1938)	AAAAA	1938
Lelystad seq (14975 – 15101)	AAAAA	15101

FIG. 11

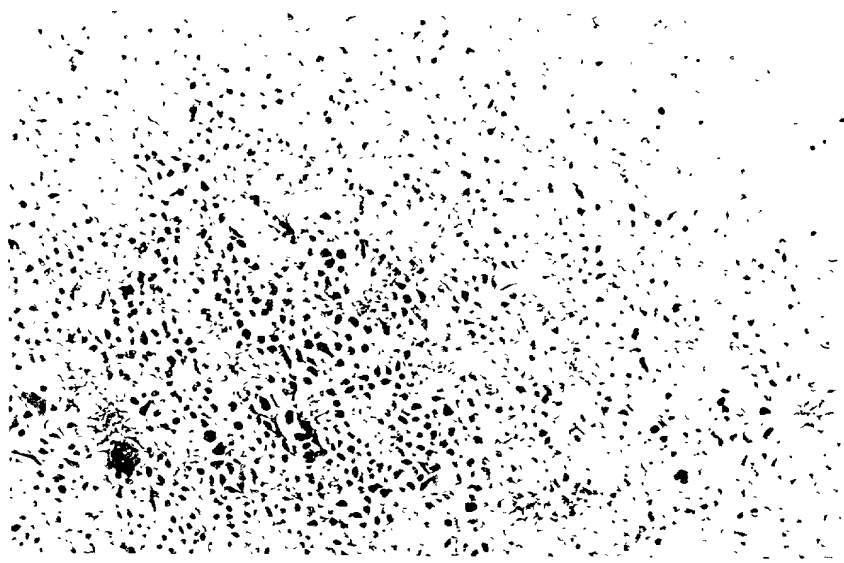


FIG.12

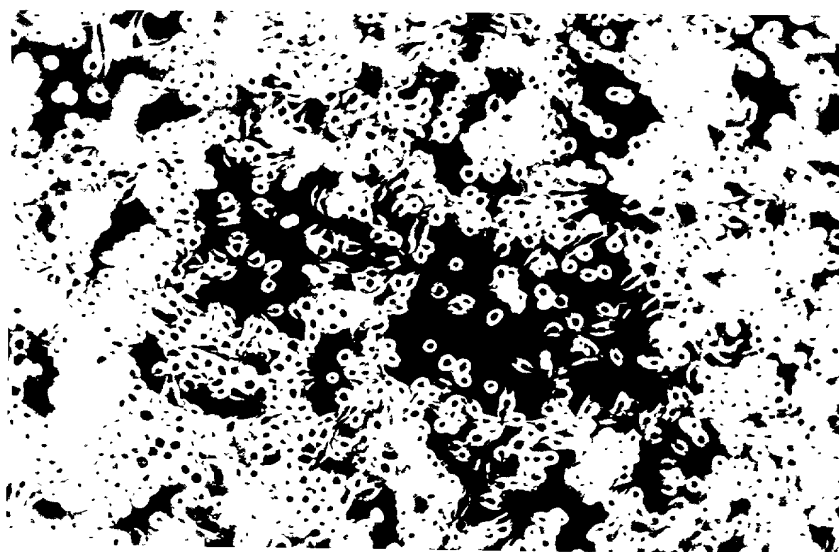


FIG.13

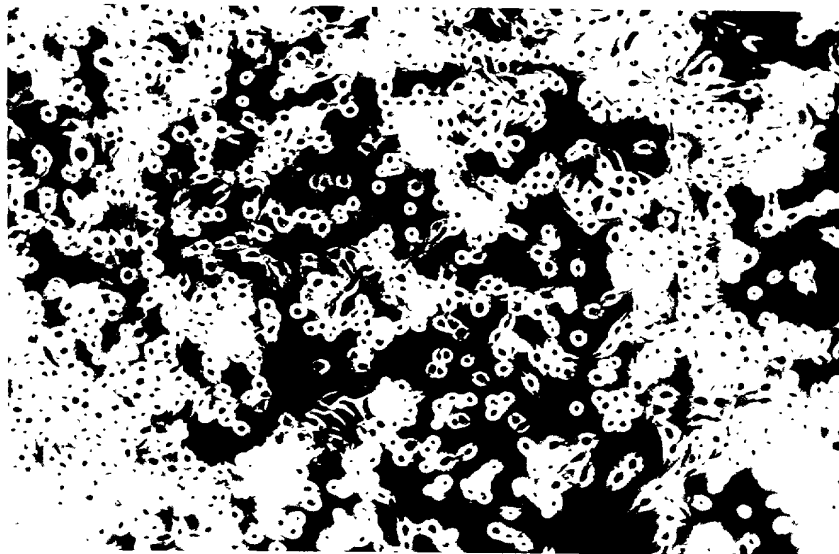


FIG.14

SM E M NP E+M+NP SM

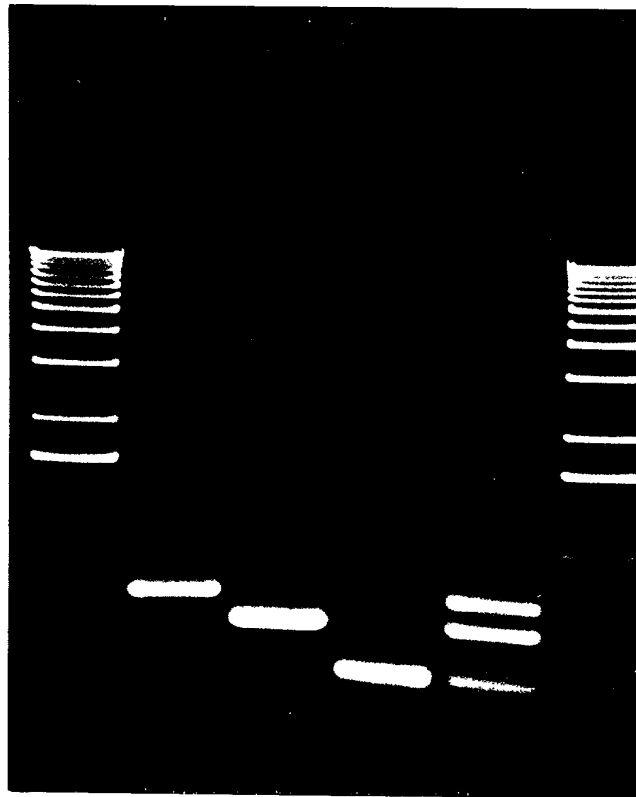


FIG.15

SM pVL1393 E M NP SM

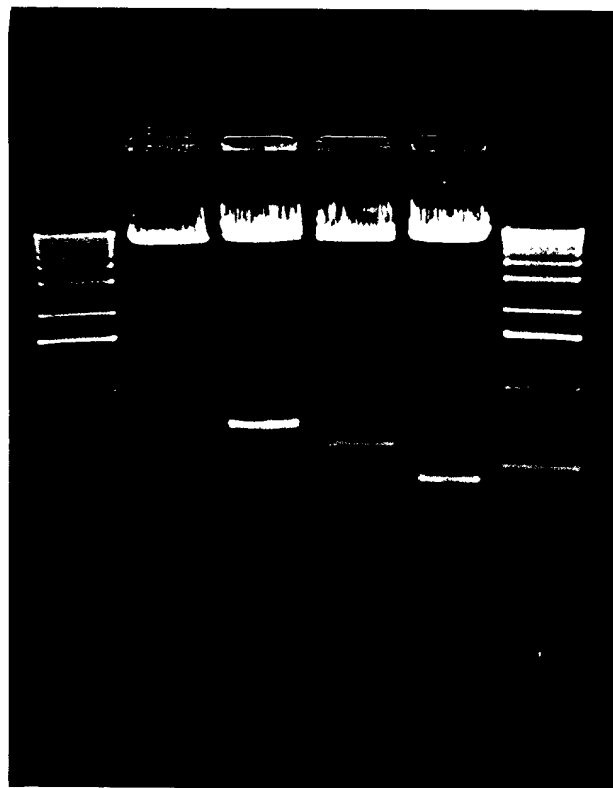


FIG.16

VR 2385	GTTTGTGCTTGCTAGGCCGAAGTACATTCTGGCCCTGCCACCACGTTGAAAGTGCCGCAGGCTTTCATCCGATTGCGGCAAAATGATAACCACGCGATT	398
ISU-1894	398
ISU-22	398
ISU-79	398
ISU-55 T..... A.....	398
ISU-3927 G.....	398
LV	A..... T.GC.. T..... GCGA..... T..... A..... TC.C... T.A.. CT.A.. GTC.. G..... GA.... A	395
VR 2385	TGTGTCGGGGCTCCCGGCTCCACTAGGTCACCGGCACATTGGTGCCCGGGTTAAAAAGCCTCGTGTGGGTGGCAGAAAAGCTGTTAAACAGGGAGTG	498
ISU-1894 G.....	498
ISU-22 T..... G.....	498
ISU-79 G.....	498
ISU-55 T..... G..... C.....	498
ISU-3927 T..... G.G..... A..... G.....	498
LV	C.CT.. GA.AAAG..... ACTA.. AT.A.. G..... TC.A.. A.. A.. AC.TCGG..... C..... C..... A.CG..... GA.....	495
<div style="text-align:center;">DRF 7 start</div>		
VR 2385	+ 1> *** DRF 6 stop GTAAACCTTGTTAAATATGCCAAAATAACACCGGCA-AGCAGCAGAGAGAGAAAGAA-----GGGGGATGGCCAGCCAGTCAATCAGCTGTG	582
ISU-1894 C..... A..... -.....	582
ISU-22 C..... A..... T.-.....	582
ISU-79 C..... A..... -.....	582
ISU-55 A..... A..... -..... A.....	582
ISU-3927 A..... A..... -..... A.....	582
LV T..... C.C.G... G.CGG.. A.A.. --.G... --.A..... AAGTACAGCTCCGAT..... A..... A..... AAAAAAAAAAAAAAAAAAAA	591

VR 2385	CCAGATGCTGGGT--AA-GATCATCGCTCACC AAAACCAGTCCAGAGGCAAGGACCGGGAAGAAAAATAAGAAAGAAACCCGGAGAGCCCCATTTC	679
ISU-1894--..-.....G.....C.....T.....	679
ISU-22C--..-.....G....T.....	679
ISU-79--..-.....C..G.....T.....	679
ISU-55--..-.....G.....C.....	679
ISU-3927	...A.....--..-.....C..G.....T.....	679
LVT.....GC..T...A AGT.C..G.---G....-..-..CCT.G....-..GCC..A.....G..T.....A.....T	679

VR 2385	CCTCTAGCGACTGAAGATGATGTCAGACATCACTTTACCCCTAGTGAGGTCATTGTTCTGTCGTCATCCAGACCGCCTTTAATCAAGGGCTGGGA	779
ISU-1894C.....G.....	779
ISU-22G.....	779
ISU-79G.....A..T.....	779
ISU-55C..T..G.....G.....A.....A.....	779
ISU-3927C.....C.....G.....T.....G.....	779
LV	..C..G..TG.....CA..C..G..C..C...AG.C...A..CTCCC.C..CT..CAA..G.....G..T..C.....A..A..	779

FIG. 17C

Accession	Sequence	Position
VR 2385	CTTGACC-CTGTCAGATTTCAGGGAGGATAAGTTACACTGTGGAGTTAGTTTGCTACGCATCATACTGTGGCCTGATCCGGGTCACAGCATCACCC-	877
ISU-1894-.....A.....T.....	877
ISU-22-.....	877
ISU-79-.....T.....	877
ISU-55T.....G.....G.....	877
ISU-3927	..C..T..T..A.....G.....T.....G.....G.....G.....	877
LV	..-..GT..G..T...TCCAGC...A..G..C...TTCAG..T.....TGC....GGTTGC.....A.....T.....G..TT..TA..T..G	878

VR 23 85	TCAG-CA-----TGA	*** □RF 7 stop
ISU-1894 ,	, , , , -, - - - - , , ,	886
ISU-22	, , , , -, - - - - , , ,	886
ISU-79	, , , , -, - - - - , , ,	886
ISU-55	, , , , -, - - - - , , ,	886
ISU-3927	, , , , -, - - - - , , ,	886
LV	C , , , T , GGGTGCAGT , A ,	898
	^ ^ ^ ^ ^ ^ ^ ^ ^ ^	

FIG. 17D

VR 2385 DRF6 MESSLDFCHDSTAPQKVLLAFSITYTPVMIYALKVSRGRLLGLLHLLVFLNCAFTFGYMTFVHFQSTNKVALTMGAWALLWGVYSAIETWKFITSRCR 100
 ISU-1894 DRF6 , G.....I..... 100
 ISU-22 DRF6 , G.....I..... 100
 SIU-55 DRF6 , G.....I..... 100
 ISU-79 DRF6 , G.....Y.....M..... 100
 ISU-3927 DRF6 , G.....N.....I.....E...R..... 100
 LV DRF6 , G-G.....N.PI.A.,LV.....I.....S.....Y.....R...L.....FT,S..... 99
 PRRSV-10 DRF6 , G-G.....N.PI.A.,LV.....I.....S.....Y.....R...L.....FT,S..... 99
 LDV-C DRF2 , G-G,-E.,DQTSWY,-IFI.,L.....IA.,S.,F.,T.A.IVNIFI.,I.,CVS.V,LMYH,-SV.,TI.,SL.,I.,V.,I.,TLVKIVDWLVI,... 96
 LDV-P DRF2 , G-G,-E.,DQTSWY,-I.,I.,L.....IA.,S.,F.,T.A.IVNIFI.,I.,CVS.V,LMYH,-SV.,T.,SL.,I.,V.,I.,TLVKIVNMWVL,... 96

VR 2385 DRF6 LCLLGRKYILAPAHHVESAAGFHPAANDNH-----AFVRRPGSTTVNGTLVPGLKSLVLGGRKAVKQGVVNLVKY-AK 183
 ISU-1894 DRF6 , 174
 ISU-22 DRF6 , 174
 SIU-55 DRF6 , 174
 ISU-79 DRF6 , 174
 ISU-3927 DRF6 ,R.....K..... 174
 LV DRF6 , C...R.....L,S,S,SG,R-----YA,K,L,S.....R.....KR.,R.....-GR 173
 PRRSV-10 DRF6 , C...R.....L,S,S,SG,R-----YA,K,L,S.....R.....KR.,R.....-GR 173
 LDV-C DRF2 , F...S.....PS.,D-----TSDGRQSLTTSITI.,K.,L.,Q.,DFQR.,K.,SK,A.,L.,VS., 171
 LDV-P DRF2 , F...S.....PS.,D-----TSDGRQSLTTSITI.,K.,L.,Q.,DFQR.,K.,SK,A.,L.,VS., 171

FIG. 18A

VR 2385 DRF7 MPNNTGQQRKK-----GDGPVNQLCQMLGKIIAHQNSRGKGPCKKKNKKNPEKHPFLATEDDVRHHFTPSERQLCLSSIQTAFNQGAGTCTLS 100
 ISU-1894 DRF7N.....Q..... 93
 ISU-22 DRF7N.....Q..... 93
 ISU-79 DRF7N.....Q..... 93
 ISU-3927 DRF7N.....K.....Q.....I.. 93
 ISU-55 DRF7N.....K.....Q.....SG..... 93
 VR2332 DRF7N.....TEE.....Q..... 93
 LV DRF7 ---A..N..SQ..KKSTAPM..N.....L..AM..KS..R---QPR..GQA.....A..I...L..QT...S...Q.....AS... 94
 PRRSV-10 DRF7 ---A..N..SQ..KKSTAPM..N.....L..AM..KS..R---QPR..GQA.....A..I...L..QT...S...Q.....PS... 94
 LDV-C DRF1 ..SQ..KK..GGQN.....AN.....N..LISALLRNAG---N..K..Q..K...-Q..-L...M..GPS..L...VM...N..V..M..R..LV..L...G..Q...V 85
 LDV-P DRF1 ..SQ..KK..SGQN.....AN.....N..LINALLRNAG---N..K..Q..K...-Q..-L...M..GPS..L...VM...N..V..M..R..LV..L...G..Q...V 85
 EAV DRF7 .ASRRSRP..AASF-----RN..R--RRQPTSNDLLRMFG.....-MRVR..PPAQPTQAI..EPG..L...DLNQQ...ATLS..NV..RF..MI..H..SL..-A 83

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VR 2385 DRF7 DSGRISYTFEFLPTHTVRLIRVTASP----SA 134
 ISU-1894 DRF7 123
 ISU-22 DRF7 123
 ISU-79 DRF7 123
 ISU-3927 DRF7P..... 123
 ISU-55 DRF7 123
 VR2332 DRF7 123
 LV DRF7 S..KV..FQ...M..VA.....STSASQGAS 128
 PRRSV-10 DRF7 S..KV..FQ...M..VA.....STSASQGAS 128
 LDV-C DRF1 ...G..NF...S..M...A.....NAS..NS----- 115
 LDV-P DRF1 ...G..NF...S..M...A.....NAS..NS----- 115
 EAV DRF7 .A..GLT...SW-V..KQIQ..KVAPP..G.....- 110

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FIG. 18B

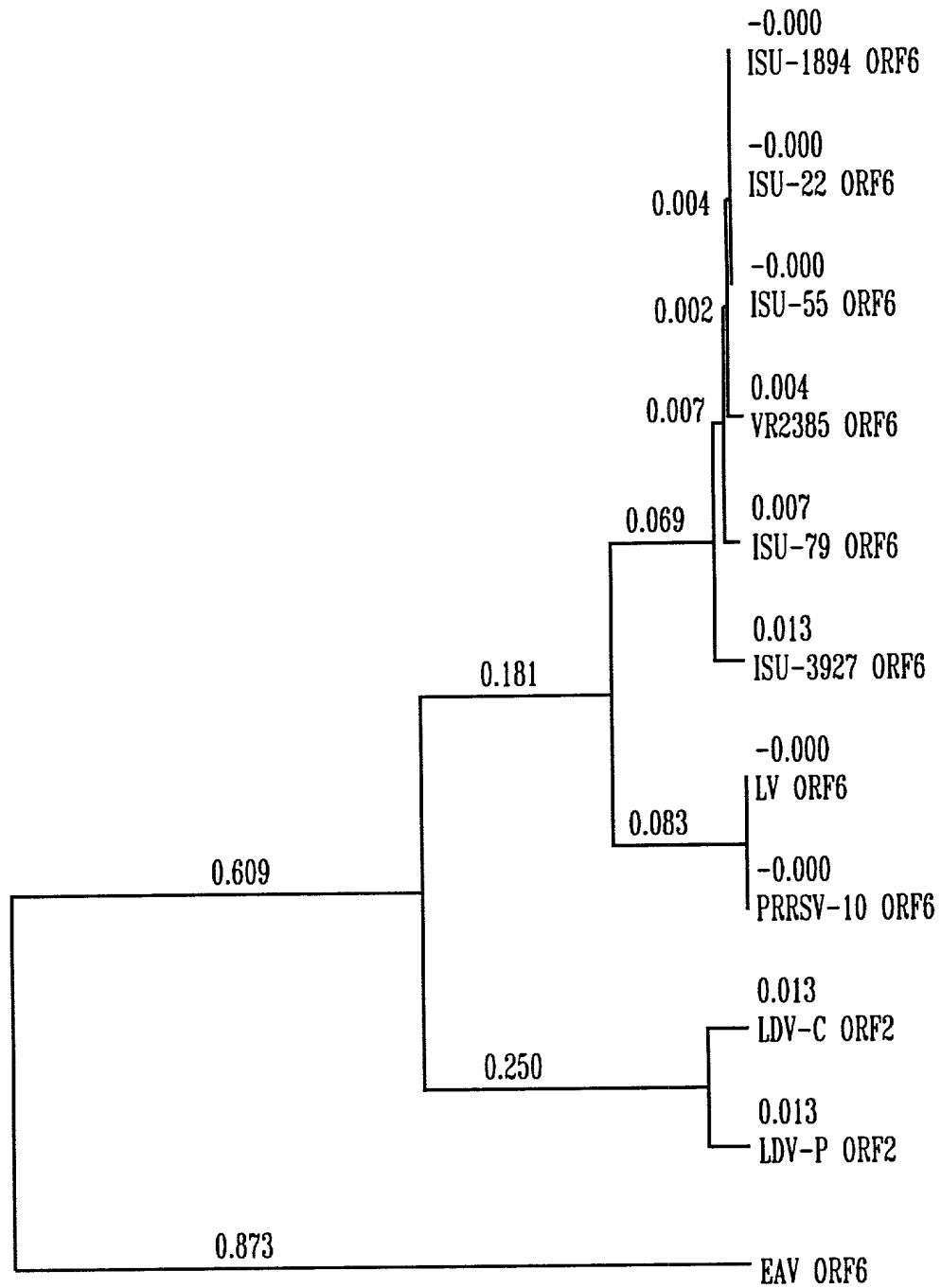


FIG. 19A

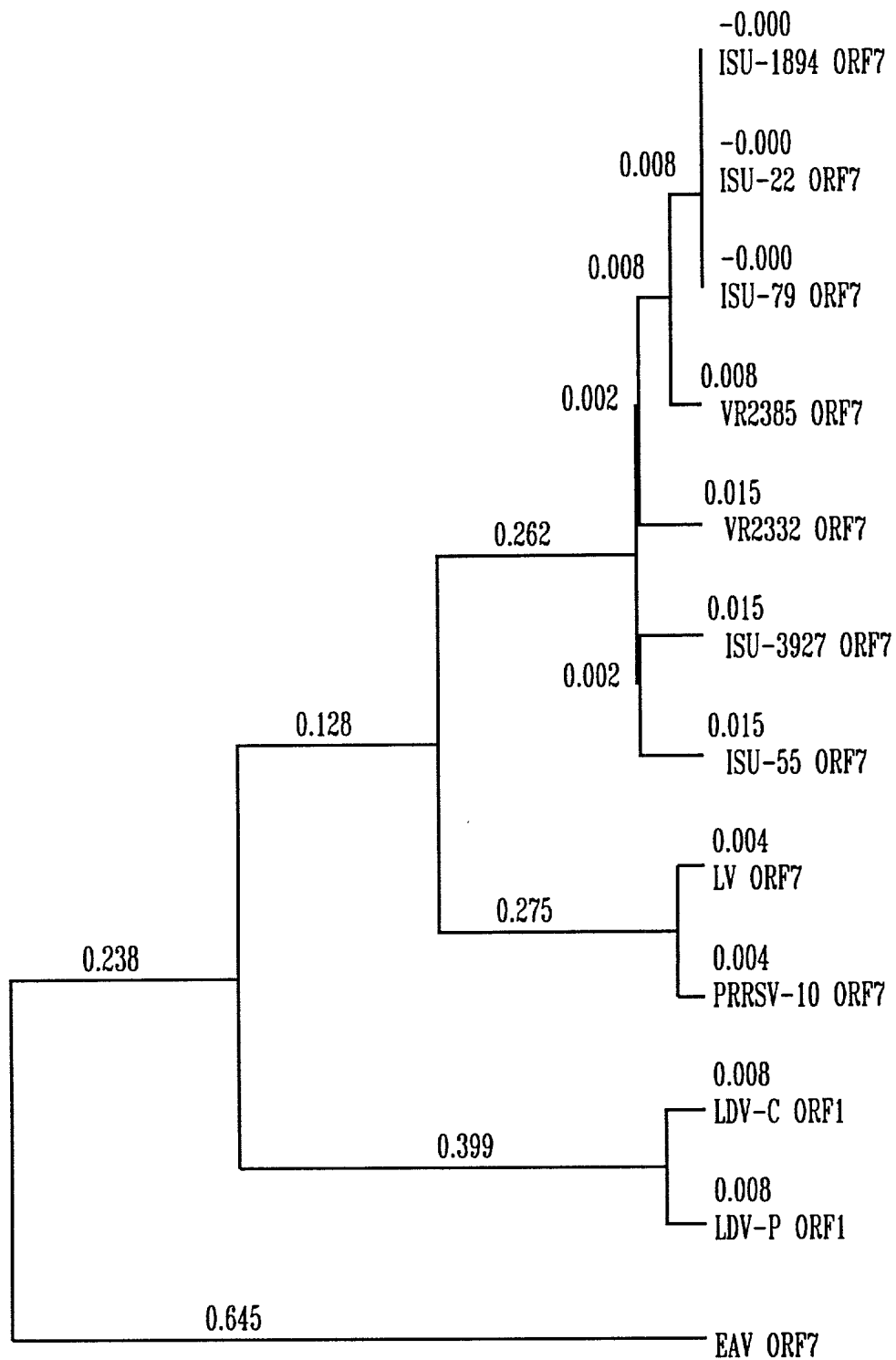


FIG. 19B

+ Start DRF2
 CCTGAATTGAGATGAGGATGCGGCTATGCAAGCCTTTTGACAAAATGGCCAACTTTTTGTGGATGCTTTCACGGAGTTCTTGGTGTCCATTGTTGAT 100
 ATCATTATATTTTTGGCCATTTGTTGGCTTCACCATCGCAGGTTGGCTGGTGGCTTTTGGCATCAGATTGGTTGGCTCCGGGATACTCCGTGGCGGCG 200
 CTGCCATTCACTCTGAGCAATTACAGAAGATCCTATGAGGCCTTTCTCTCAGTGCCAGGTGGACATTCACCCTGGGGAACTAAACATCCTTTGGGGA 300
 TGCCTTGGCACCATAAGGTGTCAACCTGATTGATGAATGGTGTGCGTGAATGTACCGCATCATGGAAAAAGCAGGACAGGCTGCCCTGGAAACAGGT 400
 AGTGAGCGAGGCTACGCTGTCTCGCATTAGTAGTTGGATGTGGTGGCTCATTTTCAGCACTTGGCGCCATTGAAGCCGAGACCTGTAAATATCTGGCC 500
 TCTCGGCTGCCCATGCTACACCACCTGCGCATGACAGGTCAAATGTAAACCATAGTGTATAATAGTACTTTGAATCAGGTGTTTGGCTGTTTCCCAACCC 600
 CTGGTCCCGGCCAAAGCTTCATGATTTCCAGCAATGGCTAATAGCTGTACATTCCTCTATATTTTCCCTGTGTGCAGCTTCTTGTACTCTTTTGTGT 700
 + Start DRF3
 GCTGTGGTTGCGGGTTCCAATGCTACGTACTGTTTTTGGTTTCCGCTGGTAGGGGCAATTTTCTTTCGAACTCAGGTTGAATTACACGGTGTGGCGC 800
 CTTGCCCTACCCGGCAAGCAGCGCCAGAGGCCCTACGAACCCGGCAGGTCCCTTTGGTGCAGGATAGGGCATGATCGATGTGGGAGGACGATCATGATGA 900
 ACTAGGGTTTGTGTGGCTCTCGGCTCTCCAGCGAAGGCCACTTGACCAGTGTCTACGCCGTGGTGGCGTCCCTGTCCCTTCAGCTATACGGGCCAGTTT 1000
 CATCCCGAGATATTCGGGATAGGGAATGTGAGTCGAGTCTATGTTGACATCAGCACCAATTCATTTGGCGTGTTCATGATGGGAGAACACCACCTTGC 1100

*** Stop DRF2

FIG. 20A

+ Start DRF4
 CCCACCATGACAACATTTACGCCGTGCTTCAGACCTATTACCAGCATCAGGTCGACGGGGGCAATTGGTTACCTAGAATGGTGCGCTTCCTTCTTTC 1200
 CTCCTGGTTGGTTTTAAATGTCCTCTGGTTCTCAGGGCTTCGGCTGCAAGCCATGTTTCAGTTCGAGTCCTTCAGACATCAAGACCACACACCACCGCAG 1300
 *** Stop DRF3
 CGGCAGGCTTTGCTGTCCCTCCAAGACATCAGTTGCCTTAGGCATCGCAACTCGGCCCTCTGAGGCGATTGCAAAAGTCCCTCAGTGGCGCAGCGGATAGG 1400
 GACACCCGTGTATACACTGTCACAGCCCAATGTTACCGATGAGAATTATTGGCATCCCTCIGATCTTCATGCTTTCCTTCCTTCCTTCATGCTTCT 1500
 GAGATGAGTGAAAAGGGATTTAAGGTGGTATTGGCAATGTGTGAGGCATCGTGGCAGTGTGGGTCAACTTACCAGTTACGTCCAACATGTCAAGGAAT 1600
 TTACCCAACGTTCCCTTGGTAGTTGACCATGTGCGGGCTGCTCCATTTTCATGACGCCCGAGACCATGAGGTGGGCAACTGTTTTAGCCIGCTTTTTTACCAT 1700
 *** Stop DRF4 + Start DRF5
 TCTGTTGGCAATTTGAATGTTAAGTATGTTGGGGAAATGCTTGACCGCGGGCTGTTGCTCGCAATTGCTTTTTTATGGTATCGTGCCGCTTGTT 1799

FIG. 20B

Consensus	ATGMAATGGGGTCWMTGYRRAGCCTTTTGAYAAAAATYRGCARCTKTTYGTGGAYGCTTCACKGAGTTCYTKGKWSYRTKGTGATATYRYATWTT	100
VR2385 DRF2	...A...TA...CAA...C...TG...A...T...T...T...G...GTCCA...T...CATT...A...	100
LV DRF2	...C...AC...TGG...-----T...CA...G...C...C...T...TAGTG...G...TGC...T...	91
Consensus	YYTKGCCATWYTGTTGGSTTACCRTCCAGGWTGGYTRSTGGTCTTYKYMTCAGAKTGTTGTCCGGGMTWCTCCGTCGGCGCYCTGCCATTAC	200
VR2385 DRF2	TT...G...TT...C...A...T...C...GG...TGCA...T...A...G...C...	200
LV DRF2	CC...T...AC...G...G...A...T...AC...CTTC...G...C...T...T...	191
Consensus	TCTSMSSAAYTAYMGAAGRTCCATGARGSCCTKYTSYCYMASTGCMRRSYGGAYAKTCCACAMTKKGSARYAARCAAYCCWTTGGGKATGYTTGGCA	300
VR2385 DRF2	...GAGC...T...CA...A...G...C...TC...CT...TC...G...CAGGT...C...T...-C...GG...G...ACT...A...T...T...G...C...	299
LV DRF2	...CCCG...C...TC...G...A...G...GT...GC...CA...C...AGACC...T-G...A...TT...C...GTC...G...C...A...T...T...	290
Consensus	CCATRMGAGTKTCMMMYCTGATTGATGARATGGTSTCKCGTCGMATKTACCRSAYCATGGAAWKCAGGWCARGCKGCTGGAAARCAGGTGTRGTRGYGA	400
VR2385 DRF2	...AA...G...AAC...C...A...G...G...A...G...GC...T...A...AG...A...G...T...A...A...A...GA...C...	398
LV DRF2	...GC...T...CCA...T...G...C...T...C...T...AG...C...T...T...T...A...G...G...G...G...T...G...T...	389
Consensus	GGCYACGCTSTCWCMAKYWGTGAGGKYTSGATRTGTRGTRKCTCATTTTCARCACTKGGCGCMRTKGARGCSGAKWCYTGYNMTWTCTSRSCCTCWGRC	500
VR2385 DRF2	...T...G...T...C...TTA...-...-...TT...G...G...G...G...T...T...G...T...CA...T...A...C...GA...C...TAAA...A...GGC...T...G...	496
LV DRF2	...C...-...C...A...A...GCT...GC...C...A...A...TA...C...A...C...G...AG...G...G...T...T...T...CCGC...T...CAG...A...A...	487

FIG. 21A

[illegible]

FIG. 21A. 1

Consensus	ATGGCTMATMRSTGTRCAYKCYTCYATWTTTCCCTCTGCTGCKWKCWTCTKKTACYYTKTYRTWTGCTGTGGYTKCGRRTTCCARYKCTACGYWMTGTT	100
LV DRF3C..CAG...G..CG..T..C..T.....G..TT..A...GT...CT..G..CA..A.....T...C..T..AA.....GCT.....CTA....	100
VR2385 DRF3A..AGC...A..TT..C..T..A.....T..AG..T...TG...TC..T...TG..T.....G...T..G..GG.....ATG.....TAC....	100
Consensus	TTTGGTTTCCRYTGGYMRSGGCAAYWWTCTTCGARTSACSRTSAAYTACACSRTRTGCWYGCCYTGYYACCMGKCAAGRGCTCGCMRARGSCT	200
LV DRF3AT...CCCAC.....CACAA..A.....G..G..CA..C.....CA..A..AT...C..TTCT...A..T.....G.....CA..A..G..	200
VR2385 DRF3GC...TTAGG.....TTTT..T.....A..C..GG..G..T.....GG..G...CC...T..CCTC...C..G.....A..-...AG..G..C..	199
Consensus	ACGARCCCGGMYGKWMCMTKTGTGTCARRATAGGGCATGAYMGRGTGTGRGGAGSRYGAYCATGATGARYTAGKKWWTGTCSRTSCCGTCYGGSYWCKMCA	300
LV DRF3	...G.....TC..TAA..A..G.....AA.....CA..G...A...CGT..C.....GT..-..TTAA.....CA..C.....C..GTA..GA..	298
VR2385 DRF3	...A.....CA..GTC..C..T.....GG.....TC..A...G...GAC..T.....AC...GGTT...-GG..G.....T..CCT..TC..	298
Consensus	sRCGAMKSMMACTTGACSRGTKMTTAYGCTGGYTGCGKTYYYTGCTTYWCTAYRCGGCCARTTCCATCCSGAGWTRTTCGGGATAGGGAATGTGWS	400
LV DRF3	A..-CTCAA.....-GG..TA...T..T...C...T..TTT.....TTC...CG.....A.....G...T..G.....TC	395
VR2385 DRF3	G...AGGCC.....CA..GC...C..C...T...G..CCC.....CAG...TA.....G.....C...A..A.....AG	398
Consensus	KCGMGTCTWYGTGACAWSMRRACCACTTCATTGCGYGVKCATGATGRCASAAAYWCMACCKTRYCYMMSRWSACAATYTCMGCMKTRYVTSMG	500
LV DRF3	G..C...TC...G...AGCGA.....G.....T..C..AG.....A..C...TT..A...G..AT..TAC..GGAC.....C...C...AT..ATA..GC..	495
VR2385 DRF3	T..A....AT..T...TCAAG.....A.....C..T..TT.....G...G...CA..C...T..GC..CCA..CATG.....T...A...CG..GCT..CA..	498

FIG. 21B

Consensus	RCMTATTACCASCAYCARRTMGACGGGGCAATTGGTTCAYYTRGAATGGSTGGCKCMYCTCTTTCYTCYTGGYTGGTKYTMAYRTMTCWTGGTTTC	600
LV DRF3	G. A. C. . C. . AA. A. C. . TT. G. C. G. . AC. T. . C. C. GC. C. CA. A.	595
VR2385 DRF3	A. C. G. . T. . GG. C. T. . CC. A. G. T. . CT. C. . T. T. . A. TG. C. . T.	598
Consensus	TSAGGCGTTCGCCTGYAAGCCMTGTTTCWSKWCGMRCTCTWTCAGAYATYRAGACCAACACSACCGCRGCKGCMGGYTTYRYKGTCTCYCARGACATCART	700
LV DRF3	. G. T. C. TCGA. . CA. A. T. . TG. G. G. . T. . C. . T. CATG. T. . G. A.	695
VR2385 DRF3	. C. C. A. AGTT. . AG. T. C. . CA. C. A. . G. . A. . C. TGCT. C. . A. G.	698
Consensus	TGYYTYMGRCMTCACGGSRWCTCRGCAGCKCAWGAGRMRAITTCCTTCGSAAGTCGYCYCARTGCGYGAMGSCGWYRGTACTCCCCAGTACATCACGA	800
LV DRF3	. . TT. CC. A. C. GGT. A. G. AAA. G. T. . C. . A. . T. A. . C. TCG.	795
VR2385 DRF3	. . CC. TA. G. A. CAA. G. T. . -T. GCG. C. -C. T. . G. . C. . C. . -C. . G. . ATA.	765
Consensus	TAA	803
LV DRF3	. . .	798
VR2385 DRF3	---	765

FIG. 21B.1

Consensus	M. WG. C., K., L., W., L., SL., P. CL. SPSQ. G. WSF. S. WFAPR. SVRALPFTL. NYRRSYE., L., C., D. P., KH	100
LV DRF2.	. Q., H. GV. SASCSWTPS. SSLLV. LI-----, PF., ---, Y., G., D. Y., F. E., P., GL. PN. RP. V. QFAV., .	90
VR2385 DRF2.	. K., L., --, -----AFLTK. AN-FL. MLSSSWCP. LI., YFW. F., A., V. W., A. D., Y., S., AF. SQ. QV. I. TWGT., .	93
Consensus	PLGM. WH., VS. LIDEMVSRR. Y., ME., GGAANKQVV. EATL., S. LD. V. HFQHLLAA. EA., C., L. SRL. ML., L., NV., YN. TL., V.,	200
LV DRF2. F., MR., H., I. QT., HS., G., TKL. G., I. T., V., DS. RF. S., V., KN. AV--G., SLQ., T., DR. ELI	188
VR2385 DRF2. L., HK., T., M. RI., KA., S., SRI. S., V. A., I., ET. KY. A., P., HH. RMTGS., TIV., S., NQ. FAV	193
Consensus	FPTPG. RPKL. DF. QWLI. VH. SIFSSVA. S. TLF. VLWLR. P. LR. VFGF. W., A.,	264
LV DRF2. T., T., R., S., A., S. V., I., I. A., Y., H. PT, ---THSS	249
VR2385 DRF2. S., H., Q., A., S., A. C., V., V. M., T., R. LG. IFLNSR-	257

FIG. 22A

Consensus	MA, C, ..., FLC, ..., Y, ..., A, ..., S, T, CFWFPL, GN, SFELT, NYT, C, PC, T, QAA, ..., EPGR, WC, IGHDRC, E, DHDEL, ..., PSG, ...	100
LV DRF3,	.. HQ, ARHF, ..., GFIC, LVHS, LASN, SS, L, ..., AH, T, ..., I, I, M, S, S, ..., RQRL, ..., NM, K, ..., E, R, ..., LMSI, ..., YDN	100
VR2385 DRF3,	.. NS, TFLYI, ..., CSFL, SFCC, VWAG, NA, Y, ..., VR, F, ..., V, V, P, L, R, ..., AEAY, ..., SL, R, ..., G, D, ..., GFVV, ..., LSS	100
Consensus	... L, ... YAWLA, LSFSY, AQFHPE, FGIGNSV, VD, ..., HQFICA, HDG, N, T, ..., NISA, ..., YY, HQ, DGGNWFHLEW, RP, FSSWLVLN, SWFL	200
LV DRF3,	L-K, EGY, ..., F, ..., A, ..., L, ..., F, KR, ..., E, H, S, VSTGH, ..., LYAA, H, I, ..., L, L, ..., I, ...	199
VR2385 DRF3,	EGH, TSA, ..., S, ..., T, ..., I, ..., Y, IK, ..., V, Q, T, LPHHD, ..., VLQT, Q, V, ..., V, F, ..., V, ...	200
Consensus	RRSP, S, VS, R, Q, RPT, P, ..., S, TS, ..., L, ..., R, F, ..., K, S, ...	266
LV DRF3,	..., V, P, R, IY, IL, ..., R, RLPVSW, FR, ..., IVSD, TGSQQRK, K, PSES RPNV, P, VLPSTSR	265
VR2385 DRF3,	..., A, H, V, VF, TS, ..., P, QRQALL, SK, V--A, GIATRPL, R, A-----, -LSAARR-	255

FIG. 22B

Consensus	M, A, LF, L, G, ..., VS, AFACKPCFS, ..., LSDI, TNTAAAGF, VLQDI, C, R, ..., A, E, I, ..., K, QCR, A, GTP, YIT, TANVTDE, YL, ..., DL	100
LV DRF4,	A, AT, F, A, AQHIM, E, ..., TH, ..., E, ..., M, ..., N, F, PHGVSA, Q, K, SFG, SS, ..., E, V, ..., Q, I, ..., S, YNA, ...	100
VR2385 DRF4,	G, SL, L, V, FKCLL, Q, ..., SS, K, ..., A, ..., S, L, HR--NS, S, A, R--, VP, T, I, V, ..., V, ..., N, HSS, ...	96
Consensus	LMLS, CLFYASEMSEKGFKV, FGNVSG, V, CVNFT, YV, HV, ..., TQ, ..., V, ..., RLLHF, TP, MRWAT, ACLF, ILLAI, ...	184
LV DRF4,	..., A, ..., I, ..., V, SA, ..., D, A, A, TQH, QHHL, IDHI, ..., L, SA, ..., TI, ..., A, ...	183
VR2385 DRF4,	..., S, ..., V, ..., I, AV, ..., S, Q, KEF, RSLV, DH-V, ..., M, ET, ..., VL, ..., T, ...	179

FIG. 22C

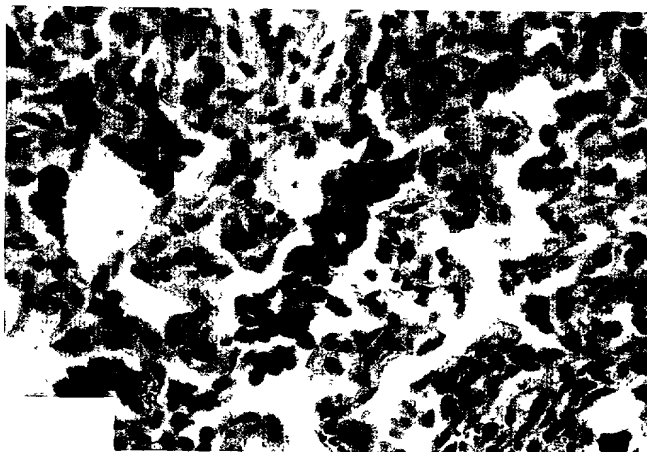


FIG.23

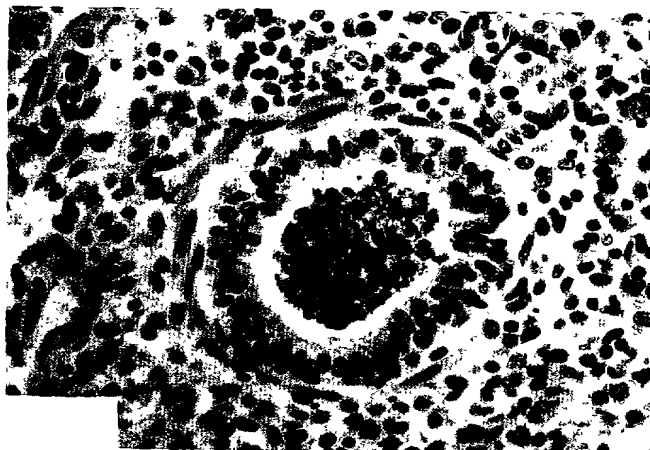


FIG.24

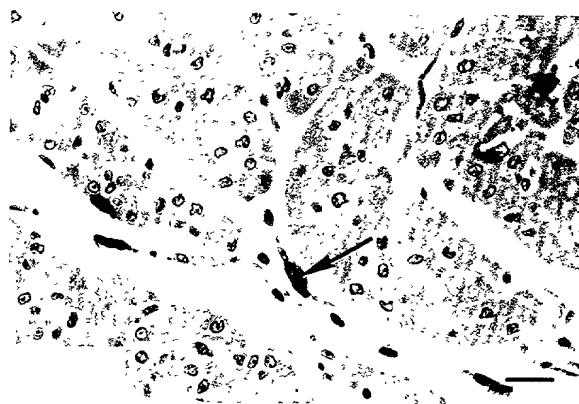


FIG.25

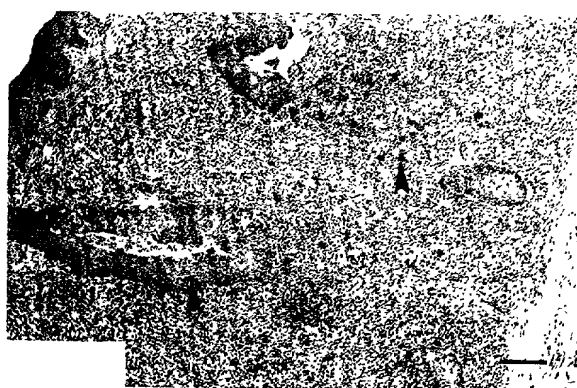


FIG.26

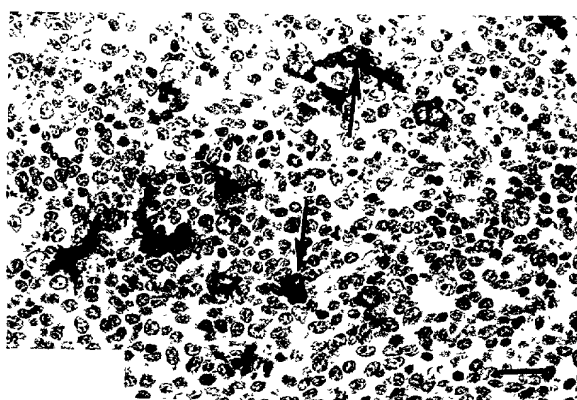


FIG.27



FIG. 28A



FIG. 28B



FIG. 28C

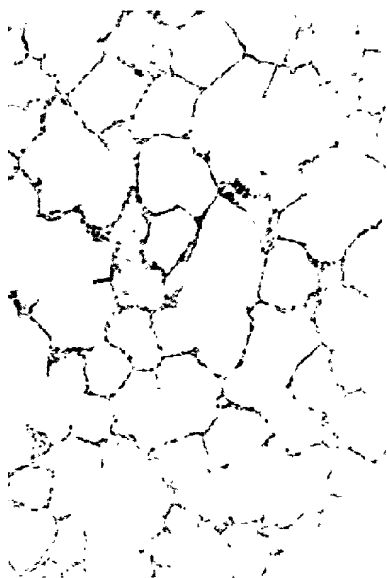


FIG. 29A



FIG. 29B



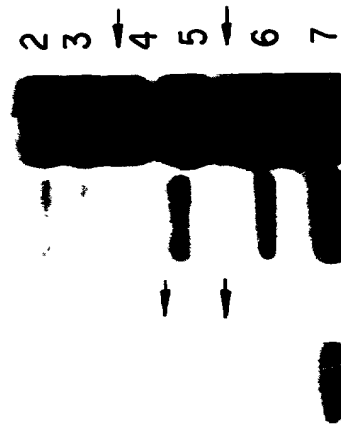
FIG. 29C

22 55 79 1894 3927



1

1



2 3 4 5 6 7



FIG.30A

FIG.30B